

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2000, 14:05:12 ; Search time 14.9 Seconds
(without alignments)
668.675 Million cell updates/sec

Title: US-09-373-230-2
Perfect score: 808
Sequence: 1 NFGRLHCTTAVIRNINDQVL.....KKDENGDKSVMTLTNLHQS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 segs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB	ID	Description
1	806	99.8	192	2	S60226	cytokine IGIF - mo
2	82.5	10.2	803	1	A64070	endopeptidase La (
3	82	10.1	267	1	JN0724	interleukin-1 beta
4	81	10.0	483	2	T21327	hypothetical prote
5	80.5	10.0	267	2	S38373	interleukin-1 beta
6	80	9.9	506	2	D71461	hypothetical prote
7	79.5	9.8	526	2	A41698	cell division cont
8	78.5	9.7	1039	2	E72734	hypothetical prote
9	78	9.7	1196	2	J01467	toxin, nontoxic co
10	78	9.7	1196	2	S46430	botulinum neurotox
11	78	9.7	1247	2	E71616	hypothetical prote
12	77.5	9.6	366	2	T30457	hypothetical prote
13	77	9.5	266	1	ICB01B	interleukin-1 beta
14	77	9.5	563	2	T09378	hypothetical prote
15	76.5	9.5	167	2	A64401	hypothetical prote
16	76.5	9.5	621	2	B64546	chaperone and heat
17	76.5	9.5	706	2	S38168	hypothetical prote
18	76.5	9.5	905	2	T39572	probable proteinas
19	76.5	9.5	1294	2	T48349	EIN2 protein - Ara
20	76	9.4	525	2	T43437	hypothetical prote
21	75.5	9.3	270	1	ICMS1	interleukin-1 alph
22	75.5	9.3	439	2	C64401	hypothetical prote
23	75.5	9.3	626	2	T35669	hypothetical AMP/G
24	75.5	9.3	695	2	T64135	carboxy-terminal p
25	75.5	9.3	866	2	T06454	probable lipoxigen
26	75	9.3	266	1	S23010	interleukin-1 beta
27	75	9.3	621	2	A71961	90kDa chaperone -
28	75	9.3	624	2	S67382	hypothetical prote
29	75	9.3	1146	2	E70204	hypothetical prote

30	74.5	9.2	270	1	S10532	interleukin-1 alph
31	74.5	9.2	661	2	S75005	senory transducti
32	74	9.2	254	2	E70230	conserved hypothet
33	74	9.2	269	1	ICH01B	interleukin-1 beta
34	74	9.2	318	2	C81447	chemotaxis protein
35	74	9.2	322	2	T48460	MADS-box protein-1
36	74	9.2	438	2	T45041	hypothetical prote
37	74	9.2	1139	2	A49370	E1A-associated cyc
38	73.5	9.1	589	2	C72414	anthranilate synth
39	73.5	9.1	647	2	S61973	hypothetical prote
40	73.5	9.1	680	2	T39858	hypothetical prote
41	73.5	9.1	1146	2	T09112	probable sensor ki
42	73.5	9.1	2077	2	T43991	large tegument pro
43	73.5	9.1	2077	2	T44178	large tegument pro
44	73	9.0	611	2	S38162	translation elonga
45	73	9.0	872	1	P2XR6W	RNA-binding protel

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OKA>
A:Cross-references: EMBL:D49949; NID:q1064822; PIDN:BAA08705.1; PID:q1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match	99.8%	Score 806;	DB 2;	Length 192;
Best Local Similarity	99.4%	Pred. No. 1.9e-65;		
Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1	NFGRLHCTTAVIRNINDQVLFDKRPVFEEDMTDIDQASASEPQTRLLIYMKDSEVRGLA 60			
DB 36	NFGRLHCTTAVIRNINDQVLFDKRPVFEEDMTDIDQASASEPQTRLLIYMKDSEVRGLA 95			
QY 61	VTLSVKDSKSTLSCKNKIISFEEMDPENIDDIQSDLIFFQKRVPGHNMKEPSSLYEG 120			
DB 96	VTLSVKDSKSTLSCKNKIISFEEMDPENIDDIQSDLIFFQKRVPGHNMKEPSSLYEG 155			
QY 121	HFLACQKEDDAFKLLKKKDENGDKSVMTLTNLHQS 157			
DB 156	HFLACQKEDDAFKLLKKKDENGDKSVMTLTNLHQS 192			

RESULT 2
A64070
endopeptidase La (EC 3.4.21.53) - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: ATP-dependent proteinase 1on; ATP-dependent serine proteinase La
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Haemophilus influenzae
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 18-Jun-1999
C:Accession: A64070
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: A64070

Db 221 --KNRVEFSALYPNMWISTSOAE 242

RESULT 6

D71461

hypothetical protein CT861 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C:Species: Chlamydia trachomatis

C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C:Accession: D71461

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:99000809

A:Accession: D71461

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <ARN>

A:Cross-references: GB:AE001359; GB:AE001273; NID:g3329331; PIDN:AAC68459.1; PID:g332933

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: CT861

Query Match

Best Local Similarity 9.9%; Score 80; DB 2; Length 506;
Matches 38; Conservative 25; Mismatches 55; Indels 34; Gaps 7;

QY 1

NEGRHCTTAVIRNINDQVLFVDKRPVEFEDMDIDQASSEPQTRLIIYMKDSEVRGLA 60

Db 63

SFSRLQPTTP-----KERILFFGS-SPSSQLSTVTRTTTSSPMN-----LFSNSQTRNST 111

QY 61

VTLVSKDSKXSTLSCKN--KIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLY 118

Db 112

RKLSERLHFSSLSARDSTKPPSSSEPIKPSENL-----LHTPEHNR-ELFSSSLK 159

QY 119

EGHFLACQKEDDAF-----KLILKKDE 141

Db 160

KDNLSPIMEEIDSFSAFTESLEERLVTQKKEE 191

RESULT 7

A41698

cell division control protein CDC55 - Yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G1345; protein YGL190c

C:Species: Saccharomyces cerevisiae

C:Date: 30-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 29-Oct-1999

C:Accession: A41698; S31274; S61128; S62055; S64207; S18513

R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; DePaoli-Roach, A.A.; Pringle, Mol. Cell. Biol. 11, 5767-5780, 1991

A:Title: CDC55, a Saccharomyces cerevisiae gene involved in cellular morphogenesis: identification

A:Reference number: A41698; MUID:92017858

A:Accession: A41698

A:Molecule type: DNA

A:Residues: 1-526 <HEA1>

A:Cross-references: GB:M72716

A:Note: the authors translated the codon TAT for residue 116 as Val and CCT for residue

R:Healy, A.M.; Zolnierowicz, S.; Stapleton, A.E.; Goebel, M.; DePaoli-Roach, A.A.; Pringle, submitted to the EMBL Data Library, July 1991

A:Reference number: S31274

A:Accession: S31274

A:Molecule type: DNA

A:Residues: 1-499, 'N', 501-526 <HEA2>

A:Cross-references: EMBL:M72716; NID:g171194; PIDN:AAA34482.1; PID:g171195

R:Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Brusch, C.V.

submitted to the EMBL Data Library, September 1995

A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cerevisiae

A:Reference number: S61128

A:Accession: S61128

A:Molecule type: DNA

A:Residues: 1-281 <BER>

A:Cross-references: EMBL:X91489; NID:g1143557; PIDN:CAA62785.1; PID:e199121; PID:g114355

R:Coglievina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bertani, I.; Brusch, C.V.

submitted to the EMBL Data Library, September 1995

A:Description: A 6.7 Kb fragment from chromosome VII of Saccharomyces cerevisiae cont

A:Reference number: S62051

A:Accession: S62051

A:Molecule type: DNA

A:Residues: 283-526 <COG>

A:Cross-references: EMBL:X91837; NID:g1177627; PIDN:CAA62954.1; PID:e203624; PID:g117

A:Experimental source: strain FY1679

R:Brusch, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64183

A:Accession: S64207

A:Molecule type: DNA

A:Residues: 1-526 <BRU>

A:Cross-references: EMBL:Z72712; NID:g1322810; PIDN:CAA96902.1; PID:e243794; PID:g132

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:CDC55

A:Cross-references: SGD:S0003158; MIPS:YGL190c

A:Map position: 7L

Query Match

Best Local Similarity 9.8%; Score 79.5; DB 2; Length 526;
Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;

QY 14

NINDQVL-FVDRKRPVEFEDMDIDQASSEPQTRLIIYMKDSEVRGLAVTLVSKDSKXST 72

Db 213

DIPOSFNIVDIKPTNMEELTEVITSAEFHPQECNLFMYSSSK-----GTIKLCDMRONS 267

QY 73

LSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAF 132

Db 268

L-CDNKTKTFFEXLDPINHN-----FFETITSSISDIKFSFN---GRYIASRD----- 311

QY 133

KLILKKDENGDSVMFTLTNMQ 156

Db 312

YLTWKIWDVNMNPKPLKTI-NIHE 334

RESULT 8

E72734

hypothetical protein ABE0413 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 17-Mar-2000

C:Accession: E72734

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339

A:Accession: E72734

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1039 <KAN>

A:Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BAAT9369.1; PID:d1043155; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0413

C:Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology

Query Match

Best Local Similarity 9.7%; Score 78.5; DB 2; Length 1039;
Matches 37; Conservative 14; Mismatches 50; Indels 39; Gaps 5;

QY 31

DMWDIDQASSEPQTRLIIYM-----YKDSEVRGLAVTLVSKDSKXSTL 73

Db 374

DIGHIDELDEEERLAIYFDKLLDDMFREELKKAQKYAEDILVGKAV-----DSKYETL 428

QY 74

SCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAF 133

Db 429

---KKILGLVLTPTPEELPDERKDLA-SQKAIVTFTEFKDTATYLYE-----K 471

Db 91 NATVYWNPIPIGEV---GVGDTREVSLLTNDLFCNEMIIIGHDIVSCFVEFRTNVN 146
QY 119 EGHFLACOKEDDAFKLILKKKDEGDKSVMTL 151
Db 147 YKLTPIEAEDPLFNLKRLRDDNNDFLLCFKL 179

RESULT 13

ICBO1B
Interleukin-1 beta precursor - bovine
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C/Accession: J10010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988
A/Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin 1-beta
A/Reference number: A94695; MUID:88318652
A/Accession: J10010
A/Molecule type: mRNA
A/Residues: 1-266 <MAL>
A/Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flagg, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A/Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A/Reference number: S01380; MUID:89016591
A/Accession: S01380
A/Molecule type: mRNA
A/Residues: 1-251, 'A', 253-266 <LEO>
A/Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C/Comment: This protein is a cytokine that mediates a variety of immunoregulatory and involved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C/Superfamily: Interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: Interleukin-1 beta #status predicted <MAT>

Query Match 9.5%; Score 77; DB 1; Length 266;
Best Local Similarity 26.0%; Pred. No. 8.9;
Matches 27; Conservative 24; Mismatches 33; Indels 20; Gaps 7;
QY 40 SEPQTRLIITYMKDSEVRG-----LAVTLVSKDKXSTLSCKNK---IISFEEMP-- 87
Db 146 SQEMNREVFCM--SFVQGERDNKIPVALGIKD-KNLYLSCVKKGDPTPTQLLEVPKV 202
QY 88 -PENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACOKEDD 130
Db 203 YPKR--NMEKRFVFFYKTEI--KNTVEFSVLYPNWYISTQIEE 242

RESULT 14

T09378
hypothetical protein F23K16.250 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C/Accession: T09378
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z16652
A/Accession: T09378
A/Molecule type: DNA
A/Residues: 1-563 <BEV>
A/Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250
A/Experimental source: cultivar Columbia; BAC clone F23K16
C/Genetics:
A/Gene: ATSP:F23K16.250
A/Map position: 4
A/Introns: 118/3; 502/3

Query Match 9.5%; Score 77; DB 2; Length 563;

Best Local Similarity 23.6%; Pred. No. 21;
Matches 33; Conservative 29; Mismatches 40; Indels 38; Gaps 7;
QY 22 VDKRQVFEDMTDIDQAS--EPQTRLIITYMKDSEVRGLAVTLVSKDS-----KXSTLS- 74
Db 329 IDKAEWVFKKMNDMNYIPSPITTECMIMYGCGSVSRAREIFEVGESEDRVLKASTLNA 388
QY 75 -----CKNKIISFEEMDPDENIDDIQSDLIFFQKRVPGHNKMEF---ESSLYEGHFLAC 125
Db 389 MEVYCRNGLY-----IEADKLF-----HNASAFRVHPDASTYKFLYKAY 428
QY 126 OKED--DAFKLILKKKDENG 143
Db 429 TKADMKEQVOYLKKMEKDG 448

RESULT 15

A64401
hypothetical protein MJ0809 - Methanococcus jannaschii
C/Species: Methanococcus jannaschii
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C/Accession: A64401
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A/Reference number: A64300; MUID:96337999
A/Accession: A64401
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-167 <BUL>
A/Cross-references: GB:U67525; GB:L77117; NID:g1591497; PIDN:AAB98817.1; PID:g1499632
C/Genetics:
A/Map position: FOR733027-733530

Query Match 9.5%; Score 76.5; DB 2; Length 167;
Best Local Similarity 26.8%; Pred. No. 5.7;
Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;
QY 47 IITYMKDSEVRGLAVTLVSKDSK-----XSTLSCKNKIISFEEMP--PENID 92
Db 38 IITYMKDSTVRIILANDDEEDKELEFKYIERLEKKDKLIEIEKIEKRLNTYIEPEGIS 97
QY 93 DIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACOKEDDAFKLILKKKDEGDKSVMTL 152
Db 98 RLSSDDI-----LELNKKIDEG-----VKYIKLIFAELEEH--KKVILEIK 136
QY 153 NLH 155
Db 137 DMH 139

Search completed: November 20, 2000, 14:07:18
Job time: 126 sec

4.